



FIG. 1

>huGST-3 (from LifeSeq EST #2617407, ORF is highlighted in capitals)

```
gaattccatt gtgttgggta cggaagacga cagaagggtg gaggagaaaa ggcgatggcc
cggctagcag tgagcctctc aaaagcagca gggaagccca agccacaagg tcttccactt
cagcacaatg ctactgccta aaaaaATGAA GCTCCTGCTG TTTCTGGTTT CCCAGATGGC
CATCTTGGCT CTATTCTTCC ACATGTACAG CCACAACATC AGCTCCCTGT CTATGAAGGC
ACAGCCCGAG CGCATGCACG TGCTGGTTCT GTCTTCCTGG CGCTCTGGCT CTTCTTTTGT
GGGGCAGCTT TTTGGGCAGC ACCCAGATGT TTTCTACCTG ATGGAGCCCG CCTGGCACGT
GTGGATGACC TTCAAGCAGA GCACCGCCTG GATGCTGCAC ATGGCTGTGC GGGATCTGAT
ACGGGCCGTC TTCTTGTGCG ACATGAGCGT CTTTGATGCC TACATGGAAC CTGGTCCCCG
GAGACAGTCC AGCCTCTTTC AGTGGGAGAA CAGCCGGGCC CTGTGTTCTG CACCTGCCTG
TGACATCATC CCACAAGATG AAATCATCCC CCGGGCTCAC TGCAGGCTCC TGTGCAGTCA
ACAGCCCTTT GAGGTGGTGG AGAAGGCCTG CCGCTCCTAC AGCCACGTGG TGCTCAAGGA
GGTGCCTTC TTCAACCTGC AGTCCCTCTA CCCGCTGCTG AAAGACCCCT CCCTCAACCT
GCATATCGTG CACCTGGTCC GGGACCCCGG GGCCGTGTTC CGTCCCCGAG AACGCACAAA
GGGAGATCTC ATGATTGACA GTCGCATTGT GATGGGGCAG CATGAGCAAA AACTCAAGAA
GGAGGACCAA CCCTACTATG TGATGCAGGT CATCTGCCAA AGCCAGCTGG AGATCTACAA
GACCATCCAG TCCTTGCCCA AGGCCCTGCA GGAACGCTAC CTGCTTGTGC GCTATGAGGA
CCTGGCTCGA GCCCCTGTGG CCCAGACTTC CCGAATGTAT GAATTCGTGG GATTGGAATT
CTTGCCCCAT CTTGAGACCT GGGTGCATAA CATCACCCGA GGCAAGGGCA TGGGTGACCA
CGCTTTCCAC ACAAATGCCA GGGATGCCCT TAATGTCTCC CAGGCTTGGC GCTGGTCTTT
GCCCTATGAA AAGGTTTCTC GACTTCAGAA AGCCTGTGGC GATGCCATGA ATTTGCTGGG
CTACCGCCAC GTCAGATCTG AACAAGAACA GAGAAACCTG TTGCTGGATC TTCTGTCTAC
CTGGACTGTC CCTGAGCAAA TCCACTAAga gggttgagaa ggctttgctg ccacctggtg
tcagcctcag tcactttctc tgaatgcttc tgagccttgc ctacatctct gagccttaac
tacatgtctg tgggtatcac actgagtgtg agttgtgtcc acacgtgctc aagcagaagg
acttttgtgt ccatgcttgt gtctagaaaa cagactgggg aaccttatgt gagcagcaca
tcccaccagt gaaacagggg attgctcttc ttcttttctt gatcttctctg tctgggcaga
cttcagagac tttgtggcct ggaggcctat taagcacgac acagtatcag tgggaattgat
ccataaacct ccctgtccac atcttgccca atggggaatg gatctttcac caaagagctc
accagcattt tccacagaga tgcgaattct gagcccttgg agttcccaat gggattcaag
gaaggaagtg ggaacaaggt tggatgccta cttatgagct tgaccataca gctatcggta
atcagaaata tgaacaacaaa tctctgacaa aagagcaagc tcttaagttc acaaggtgcc
tgggcttgat ttgaatatca tttccctttg cattttccca ttacatagaa aactttgacc
tgtgaaactt gccatctgtt aataactaaa ttcccaaata aggttctgtt tagaatgtcc
ctttttatgc ttcttaatta ttagcagtaa atgttcattt ttatgggatc ctaaaaaaaaa
aaa (SEQ ID NO: 13)
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FIG. 2

>huGST-3 (Full length EST Lifeseq #2617407)

Met	Leu	Leu	Pro	Lys	Lys	Met	Lys	Leu	Leu	Leu	Phe	Leu	Val	Ser	Gln
1				5				10						15	
Met	Ala	Ile	Leu	Ala	Leu	Phe	Phe	His	Met	Tyr	Ser	His	Asn	Ile	Ser
			20					25					30		
Ser	Leu	Ser	Met	Lys	Ala	Gln	Pro	Glu	Arg	Met	His	Val	Leu	Val	Leu
		35					40					45			
Ser	Ser	Trp	Arg	Ser	Gly	Ser	Ser	Phe	Val	Gly	Gln	Leu	Phe	Gly	Gln
	50					55					60				
His	Pro	Asp	Val	Phe	Tyr	Leu	Met	Glu	Pro	Ala	Trp	His	Val	Trp	Met
65					70					75					80
Thr	Phe	Lys	Gln	Ser	Thr	Ala	Trp	Met	Leu	His	Met	Ala	Val	Arg	Asp
				85					90					95	
Leu	Ile	Arg	Ala	Val	Phe	Leu	Cys	Asp	Met	Ser	Val	Phe	Asp	Ala	Tyr
			100					105					110		
Met	Glu	Pro	Gly	Pro	Arg	Arg	Gln	Ser	Ser	Leu	Phe	Gln	Trp	Glu	Asn
		115					120					125			
Ser	Arg	Ala	Leu	Cys	Ser	Ala	Pro	Ala	Cys	Asp	Ile	Ile	Pro	Gln	Asp
	130					135					140				
Glu	Ile	Ile	Pro	Arg	Ala	His	Cys	Arg	Leu	Leu	Cys	Ser	Gln	Gln	Pro
145					150					155					160
Phe	Glu	Val	Val	Glu	Lys	Ala	Cys	Arg	Ser	Tyr	Ser	His	Val	Val	Leu
				165					170					175	
Lys	Glu	Val	Arg	Phe	Phe	Asn	Leu	Gln	Ser	Leu	Tyr	Pro	Leu	Leu	Lys
			180					185					190		
Asp	Pro	Ser	Leu	Asn	Leu	His	Ile	Val	His	Leu	Val	Arg	Asp	Pro	Arg
		195					200					205			
Ala	Val	Phe	Arg	Ser	Arg	Glu	Arg	Thr	Lys	Gly	Asp	Leu	Met	Ile	Asp
	210					215					220				
Ser	Arg	Ile	Val	Met	Gly	Gln	His	Glu	Gln	Lys	Leu	Lys	Lys	Glu	Asp
225					230					235					240
Gln	Pro	Tyr	Tyr	Val	Met	Gln	Val	Ile	Cys	Gln	Ser	Gln	Leu	Glu	Ile
				245					250					255	
Tyr	Lys	Thr	Ile	Gln	Ser	Leu	Pro	Lys	Ala	Leu	Gln	Glu	Arg	Tyr	Leu
			260					265					270		
Leu	Val	Arg	Tyr	Glu	Asp	Leu	Ala	Arg	Ala	Pro	Val	Ala	Gln	Thr	Ser
		275					280					285			
Arg	Met	Tyr	Glu	Phe	Val	Gly	Leu	Glu	Phe	Leu	Pro	His	Leu	Gln	Thr
	290					295					300				
Trp	Val	His	Asn	Ile	Thr	Arg	Gly	Lys	Gly	Met	Gly	Asp	His	Ala	Phe
305					310					315					320
His	Thr	Asn	Ala	Arg	Asp	Ala	Leu	Asn	Val	Ser	Gln	Ala	Trp	Arg	Trp
				325					330					335	
Ser	Leu	Pro	Tyr	Glu	Lys	Val	Ser	Arg	Leu	Gln	Lys	Ala	Cys	Gly	Asp
			340					345					350		
Ala	Met	Asn	Leu	Leu	Gly	Tyr	Arg	His	Val	Arg	Ser	Glu	Gln	Glu	Gln
		355					360					365			
Arg	Asn	Leu	Leu	Leu	Asp	Leu	Leu	Ser	Thr	Trp	Thr	Val	Pro	Glu	Gln
	370					375						380			
Ile	His														
385															

(SEQ ID NO: 2)



FIG. 3

>msGST-3 from mouse C57BI/6 BAC clone #87(b15) (ORF is highlighted as capitals)

```
gggcatctaa cttacacttg gtcagacaag acaagctttt gcctacaaag gccacactct
gtcaggggtg tagaaagggt tgggggtgtg cagaactccc tatagtgatt aaatgtgctg
ggtaggatat tctcgggtgt ttgatggatg agaaagccca gaggggtgagt tttaaagact
tgtaacatag aatgcagtga tccaattaag agccagaatt actttgcaga gggatctgga
caaatacttg caggaatgtt tttgggtttt gtttggtttg ttggttggtt tacattgctc
cttggaatgg aatccagaga agcccgaagg tagatgctgt aacaacctaa ctcagcccca
tcccctctgc ttgctctttc aagggtcttc ccttcttccg caggatgatg ctgttgaaga
aaggagggtc gctgatgttc ctgggttccc aggtcatcgt tgtagctctc ttcattccata
tgtccgtcca cagacacctt tcccagaggg aggagtccag gagggccgtg catgtgctgg
tgctgtcttc ctggcggtca ggatcctctt ttgtgggaca gcttttcggg cagcaccctg
atgtgttcta cctgatggag cctgcctggc atgtgtggat gactttcacc agcagcacag
cctggaagct gcacatggct gtgcgggatc ttctgcgttc cgtcttcctg tgtgacatga
gcgtctttga tgcctacatg aaccaggcc cccggaacaa gtccagcctc ttccagtggg
agcaaagccg ggccctgtgc tcagcgctg tgtgtgactt cttccctgcc cagcagatca
gctaccccaa gcaactgcaag ctgctctgcg gtcagcagcc ctttgatatg gtggagaagg
cctgccgctc tcacggcttc gtggtactca aggaggtgcg ttttctcagc ctgcaggccc
tctatccact actcacggac ccttccctca acctgcacgt cgtgcacctg gtccgagacc
cccgggccgt gttccgatcc cgggagcaca ccaccataga actcatgggt gacagtcata
ttgtgctagg gcagcatttg gaaacgatca aggaggaaga ccagccctat tatgccatga
agatcatctg caaaagccag gtggacatag tcaaggccat ccaaaccctc cctgaagctc
tgcagcagcg ctacctgttc ctgaggtatg aggacctggt tcgggcaccc ctggcccaga
cgaccagact atataaattt gtgggggttg attttttgcc ccacctccaa acatgggttt
acaatgtcac ccgcggcaag ggcatgggtc agcatgcctt ccatactaac gccaggaacg
ccctcaacgt ctctcaggcg tggcggttgt ccttacctta cgaaaagggt tcccagcttc
aagatgcctg cgggtgaggct atggatttgc tgggatacct ccaggtcaga tctcaacaag
aacaaggcaa cctgtccctg gatcttctgt cctcctccca tatcttgggg caggtcttcc
gagaagggtta aggaggtctg tctgcacccc ttggttccag ccttagtcac cattaacgc
acagaagcct taagggtataa ccaaactgag tgccccttcc tcctcagccc caagcagagg
ggtctttgtg tctatactca tgtctaccct acaactgagc ctaaaaagcc aagaaacagt
atctttctgt cttgaaaata cttaggaacc ttaagcagcc cctttgacct gtcaagcaag
actttcttgt aaccttggcc ttcttacctg tgcatacctt ggagactcgg tctggaggca
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tctaag (SEQ ID NO: 14)
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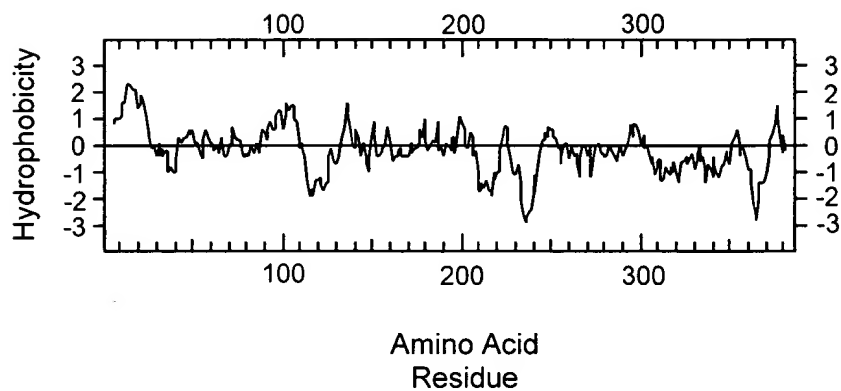
FIG. 4

Met	Met	Leu	Leu	Lys	Lys	Gly	Arg	Leu	Leu	Met	Phe	Leu	Gly	Ser	Gln
1				5					10					15	
Val	Ile	Val	Val	Ala	Leu	Phe	Ile	His	Met	Ser	Val	His	Arg	His	Leu
			20					25					30		
Ser	Gln	Arg	Glu	Glu	Ser	Arg	Arg	Pro	Val	His	Val	Leu	Val	Leu	Ser
		35					40					45			
Ser	Trp	Arg	Ser	Gly	Ser	Ser	Phe	Val	Gly	Gln	Leu	Phe	Gly	Gln	His
	50					55					60				
Pro	Asp	Val	Phe	Tyr	Leu	Met	Glu	Pro	Ala	Trp	His	Val	Trp	Met	Thr
65					70					75					80
Phe	Thr	Ser	Ser	Thr	Ala	Trp	Lys	Leu	His	Met	Ala	Val	Arg	Asp	Leu
				85					90					95	
Leu	Arg	Ser	Val	Phe	Leu	Cys	Asp	Met	Ser	Val	Phe	Asp	Ala	Tyr	Met
			100					105					110		
Asn	Pro	Gly	Pro	Arg	Lys	Gln	Ser	Ser	Leu	Phe	Gln	Trp	Glu	Gln	Ser
		115					120					125			
Arg	Ala	Leu	Cys	Ser	Ala	Pro	Val	Cys	Asp	Phe	Phe	Pro	Ala	His	Glu
	130						135					140			
Ile	Ser	Ser	Pro	Lys	His	Cys	Lys	Leu	Leu	Cys	Gly	Gln	Gln	Pro	Phe
145					150					155					160
Asp	Met	Val	Glu	Lys	Ala	Cys	Arg	Ser	His	Gly	Phe	Val	Val	Leu	Lys
				165					170					175	
Glu	Val	Arg	Phe	Leu	Ser	Leu	Gln	Ala	Leu	Tyr	Pro	Leu	Leu	Thr	Asp
			180					185					190		
Pro	Ser	Leu	Asn	Leu	His	Val	Val	His	Leu	Val	Arg	Asp	Pro	Arg	Ala
		195					200					205			
Val	Phe	Arg	Ser	Arg	Glu	His	Thr	Thr	Ile	Glu	Leu	Met	Val	Asp	Ser
	210					215					220				
His	Ile	Val	Leu	Gly	Gln	His	Leu	Glu	Thr	Ile	Lys	Glu	Glu	Asp	Gln
225					230					235					240
Pro	Tyr	Tyr	Ala	Met	Lys	Ile	Ile	Cys	Lys	Ser	Gln	Val	Asp	Ile	Val
				245					250					255	
Lys	Ala	Ile	Gln	Thr	Leu	Pro	Glu	Ala	Leu	Gln	Gln	Arg	Tyr	Leu	Phe
			260					265					270		
Leu	Arg	Tyr	Glu	Asp	Leu	Val	Arg	Ala	Pro	Leu	Ala	Gln	Thr	Thr	Arg
		275					280					285			
Leu	Tyr	Lys	Phe	Val	Gly	Leu	Asp	Phe	Leu	Pro	His	Leu	Gln	Thr	Trp
	290					295					300				
Val	Tyr	Asn	Val	Thr	Arg	Gly	Lys	Gly	Met	Gly	Gln	His	Ala	Phe	His
305					310					315					320
Thr	Asn	Ala	Arg	Asn	Ala	Leu	Asn	Val	Ser	Gln	Ala	Trp	Arg	Trp	Ser
				325				330						335	
Leu	Pro	Tyr	Glu	Lys	Val	Ser	Gln	Leu	Gln	Asp	Ala	Cys	Gly	Glu	Ala
			340					345					350		
Met	Asp	Leu	Leu	Gly	Tyr	Leu	Gln	Val	Arg	Ser	Gln	Gln	Glu	Gln	Gly
		355					360					365			
Asn	Leu	Ser	Leu	Asp	Leu	Leu	Ser	Ser	Ser	His	Ile	Leu	Gly	Gln	Val
	370					375					380				
Phe	Arg	Glu	Gly												
385															

(SEQ ID NO: 15)



FIG. 5



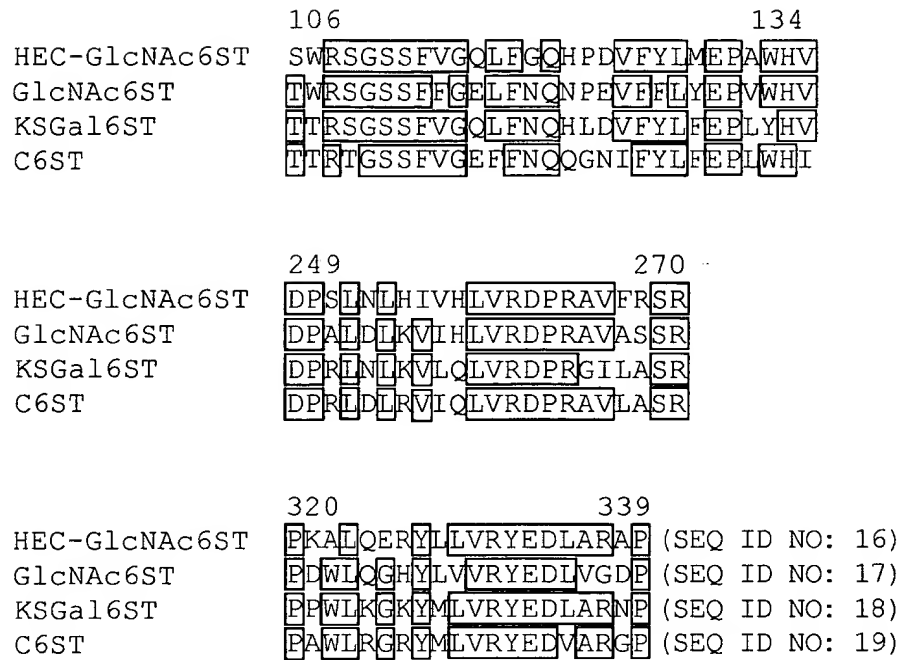
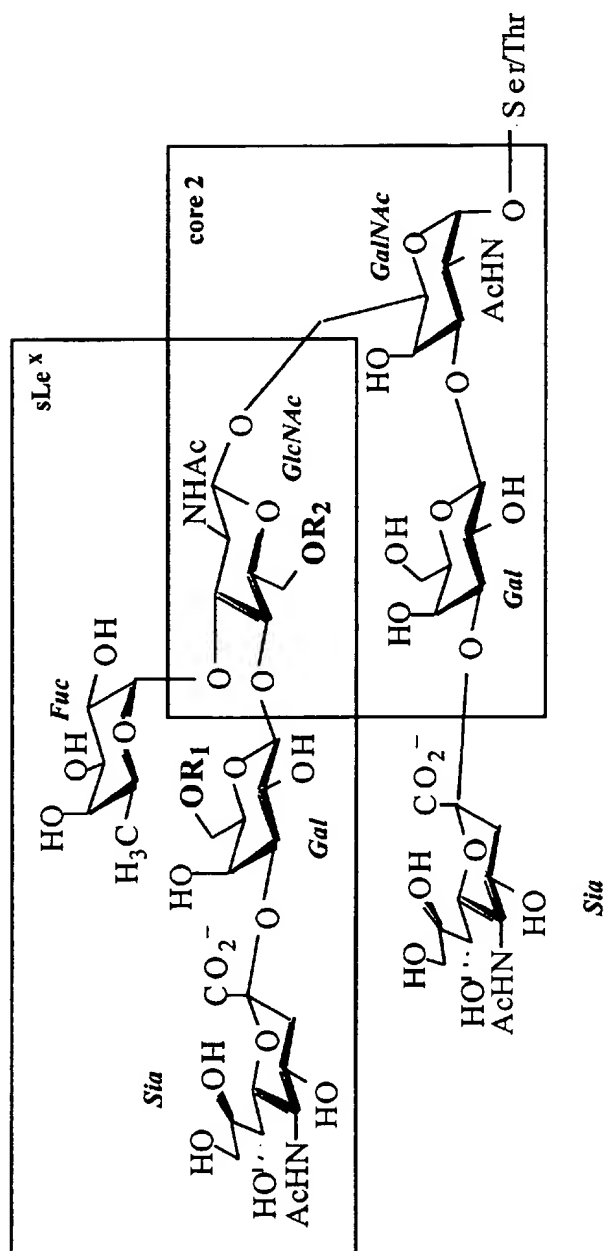


FIG. 6



R1 = H, R2 = SO³⁻ : 6-sulfo sLe^x
 R1 = SO³⁻, R2 = H : 6'-sulfo sLe^x
 R1 = R2 = SO³⁻ : 6',6-disulfo sLe^x

FIG. 7